



RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/686,234A

Source:

1600

Date Processed by STIC:

7/18/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002



Does Not Comply 1600
Corrected Diskette Needed

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/686,234A

DATE: 07/18/2002
TIME: 13:16:40

Input Set : A:\EP.txt
Output Set: N:\CRF3\07182002\I686234A.raw

SEQUENCE LISTING

2 (1) GENERAL INFORMATION:
4 (i) APPLICANT: SOMMERVILLE, CHRIS
5 SCHIEBLE, WOLF
6 (ii) TITLE OF INVENTION: MODIFIED CELLULOSE SYNTHASE GENE
7 FROM ARABIDOPSIS THALIANA CONFERS HERBICIDE RESISTANCE
8 TO PLANTS
10 (iii) NUMBER OF SEQUENCES: 2
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: PAUL A. GOTTLIEB, AGCTT
14 DEPARTMENT OF ENERGY
15 GC-62 (FORSTL) MS-6F-067
16 (B) STREET: 1000 INDEPENDENCE AVE. S.W.
17 (C) CITY: WASHINGTON, D.C.
C--> 18 (F) ZIP: 20585
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: FLOPPY DISK
22 (B) COMPUTER: IBM PC COMPATIBLE
23 (C) OPERATING SYSTEM: MS-DOS
24 (D) SOFTWARE: WORDPERFECT 8
26 (vi) CURRENT APPLICATION DATA:
C--> 27 (A) APPLICATION NUMBER: US/09/686,234A
C--> 28 (B) FILING DATE: 11-Oct-2000
31 (viii) ATTORNEY/AGENT INFORMATION:
32 (A) NAME: SMITH, BRADLEY
33 (B) REGISTRATION NUMBER: 334436
34 (C) REFERENCE/DOCKET NUMBER: S-93994
C--> 36 (ix) TELECOMMUNICATION INFORMATION:
37 (A) TELEPHONE: 630-252-2160
38 (B) TELEFAX: 630-252-2779

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

ERRORED SEQUENCES

43 (2) INFORMATION FOR SEQ ID NO: 1:
45 (i) SEQUENCE CHARACTERISTICS:
46 (A) LENGTH: 3563 NUCLEOTIDES
47 (B) TYPE: NUCLEIC ACID
48 (C) STRANDEDNESS: DOUBLE STRANDED
49 (D) TOPOLOGY: LINEAR
C--> 52 (ii) MOLECULE TYPE: cDNA
58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
E--> 60 ① atcccaagat tctctcttc gtcttcctta taaactatct ctctgtagag aagaaagctt

↑
Nucleotide numbers
must be on the right margin;
and must be a maximum
number of 60
per line
per
Sect. 1.823(a)

must be on right - max. of 2000

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↓

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E--> 61      61 ggatccagat tgagagagat tcagagagcc acatcaccac actccatctt cagatctcat
E--> 62      121 gatttgaact attccgacgt ttcggtggtg gaagcaacta agtgacaaat ggaatccgaa
E--> 63      181 ggggaaaccg cgggaaagcc gatgaagaac attgttccgc agacttgcca gatctgtagt
E--> 64      241 gacaatgttg gcaagactgt tgatggagat cgttttggg cttgtgatat ttgttcattc
E--> 65      301 ccagtttgtc ggccttgcta cgagtatgag aggaaagatg ggaatcaatc ttgtcctcag
E--> 66      361 tgcaaaacca gatacaagag gctcaaaggt agtcctgcta ttcttggtga taaagacgag
E--> 67      421 gatggcttag ctgatgaagg tactgttgag ttcaactacc ctcagaagga gaaaatttca
E--> 68      481 gageggatgc ttggttgcca tcttactcgt ggggaaggag aggaaatggg ggaaccccag
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E--> 70      601 ggagagtttt ctgctgcttc acctgaacgc ctctctgtat cttctactat cgctggggga
E--> 71      661 aagcgcttcc cctattcatc agatgtcaat caatcaccaa atagaaggat tgtggatcct
E--> 72      721 gttggactcg ggaatgtagc ttggaaggag agagttgatg gctggaaaat gaagcaagag
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E--> 75      901 tcaaggaaag tttcaattcc ttcacacagg atcaatcctt acagaatggt tattatgctg
E--> 76      961 cggettgtta tcctttgtct cttcttgcat taccgtataa caaacccagt gccaaatgcc
E--> 77      1021 tttgctctat ggetggtctc tgtgatagt gagatctggt ttgccttacc ctggattttg
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E--> 79      1141 agatatgata gtgaagggtga gccatcacag ttagctgctg ttgacatttt cgtgagtact
E--> 80      1201 gttgaccctt tgaaggagcc accccttggt acagccaaca cagtgtcttc tattctggct
E--> 81      1261 gttgactacc cagttgacaa ggtgtcctgt tatgtttttg atgatgggtg tgcattgcta
E--> 82      1321 tcatttgaat cacttgacga aacatcacag tttgtcctga aatgggtacc attttgcaag
E--> 83      1381 aaatatagca tagagcctcg tgcaccagaa tggtagcttg ctgcgaaaat agattacttg
E--> 84      1441 aaggataaag ttcagacatc atttgtcaaa gatcgtagag ctatgaagag ggaatatgag
E--> 85      1501 gaatttataa tccgaatcaa tgcacttggt tccaaagccc taaaatgtcc tgaagaaggg
E--> 86      1561 tgggttatgc aagatggcac accgtggcct ggaaataata caggggacca tccaggaatg
E--> 87      1621 atccaggtct tcttagggca aaatgggtga cttgatgcag agggcaatga gctcccgcgt
E--> 88      1681 ttggtatatg tttctcgaga aaagcgacca ggattccagc accacaaaaa ggctgggtgct
E--> 89      1741 atgaatgcac tggtagagat ttcagcagtt cttaccaatg gacctttcat cttgaatctt
E--> 90      1801 gattgtgata attacataaa taacagcaaa gccttaagag aagcaatgtg cttcctgatg
E--> 91      1861 gacccaaacc tcgggaagca agtttgttat gttcagttcc cacaaagatt tgatggtatc
E--> 92      1921 gataagaacg atagatatgc taatcgtaat accgtgttct ttgatattaa cttgagaggt
E--> 93      1981 ttagatggga ttcaaggacc tgtatatgtc ggaactggat gtgttttcaa cagaacagca
E--> 94      2041 ttatacggtt atgaacctcc aataaaagta aaacacaaga agccaagtct tttatctaag
E--> 95      2101 ctctgtgggt gatcaagaaa gaagaattcc aaagctaaga aagagtcgga caaaaagaaa
E--> 96      2161 tcaggcaggc atactgactc aactgttccct gtattcaacc tcgatgacat agaagaggga
E--> 97      2221 gttgaagggt ctggttttga tgatgaaaag gcgctcttaa tgcgcaaat gagcctggag
E--> 98      2281 aagcgatttg gacagctgac tgtttttggt gcttctaccc taatggaaaa tgggtggtgt
E--> 99      2341 cctccttcag caactccaga aaacctcttc aaagaggcta tccatgtcat tagttgtggt
E--> 100     2401 tatgaggata agtcagattg gggaaatggag attggatgga tctatgggtc tgtgacagaa
E--> 101     2461 gatattctga ctgggttcaa aatgcatgcc cgtggatggc gatccattta ctgcatgcct
E--> 102     2521 aagcttccag ctttcaaggg ttctgtcctt atcaatcttt cagatcgtct gaaccaagtg
E--> 103     2581 ctgaggtggg ctttaggttc agttgagatt ctcttcagtc ggcattgtcc tatatggtat
E--> 104     2641 gggtacaatg ggaggctaaa atttcttgag aggtttgcgt atgtgaacac caccatctac
E--> 105     2701 cctatcacct ccattcctct tctcatgtat tgtacattgc tagccgtttg tctcttcacc
E--> 106     2761 aaccagttta ttattcctca gattagtaac attgcaagta tatggtttct gtctctcttt
E--> 107     2821 ctctccattt tcgccacggg tatactagaa atgaggtgga gtggcgtagg catagacgaa
E--> 108     2881 tgggtggagaa acgagcagtt ttgggtcatt ggtggagtat ccgctcattt attcgtctgt
E--> 109     2941 tttcaaggta tcctcaaagt ccttgccggt attgacacaa acttcacagt tatctcaaaa

```

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Some error

```

E--> 110 3001 gcttcagatg aagacggaga ctttgcgtgag ctctacttgt tcaaatggac aacacttctg
E--> 111 3061 attccgccaa cgacgctgct cattgtaaac ttagtgggag ttgttgcagg agtctcttat
E--> 112 3121 gctatcaaca gtggatacca atcatgggga ccactctttg gtaagtgtgt ctttgccttc
E--> 113 3181 tgggtgattg ttcacttgta ccctttcttc aagggttga tgggtcgaca gaaccggact
E--> 114 3241 cctaccattg ttgtggtctg gtctgttctc ttggcttcta tcttctcggt gttgtgggtt
E--> 115 3301 aggattgac ccttcactag ccgagtcact ggcccggaca ttctggaatg tggaaatcaac
E--> 116 3361 tgttgagaag cgagcaaata tttacctgtt ttgagggtta aaaaaaacac agaatttaaa
E--> 117 3421 ttatttttca ttgttttatt tgttcacttt tttacttttg ttgtgtgtat ctgtctgttc
E--> 118 3481 gttcttctgt cttggtgtca taaatttatg tgtagaatat atcttactct agttactttg
E--> 119 3541 gaaagttata attaaagtga aag

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124 (2) INFORMATION FOR SEQ ID NO: 2:

126 (i) SEQUENCE CHARACTERISTICS:

127 (A) LENGTH: 3563 NUCLEOTIDES

128 (B) TYPE: NUCLEIC ACID

129 (C) STRANDEDNESS: DOUBLE STRANDED

130 (D) TOPOLOGY: LINEAR

132 (ii) MOLECULE TYPE: cDNA

134 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Some error

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E--> 136 1 atcccaagat tctctcttc gtcttcttta taaactatct ctctgtagag aagaaagctt
E--> 137 61 ggatccagat tgagagagat tcagagagcc acatcaccac actccatctt cagatctcat
E--> 138 121 gatttgaact attccgacgt ttcggtgttg gaagcaacta agtgacaaat ggaatccgaa
E--> 139 181 ggggaaaccg cgggaaagcc gatgaagaac attgttccgc agacttgcca gatctgtagt
E--> 140 241 gacaatgttg gcaagactgt tgatggagat cgttttgggt cttgtgatat ttgttcattc
E--> 141 301 ccagtttgtc ggccttgcta cgagtatgag aggaaagatg ggaatcaatc ttgtcctcag
E--> 142 361 tgcaaaacca gatacaagag gctcaaaggt agtctctgta ttctgttgta taaagacgag
E--> 143 421 gatggcttag ctgatgaagg tactgttgag ttcaactacc ctcaagaagg gaaaatttca
E--> 144 481 gagcggatgc ttggttgga tcttactcgt gggaaggagg aggaaatggg ggaacccag
E--> 145 541 tatgataaag aggtctctca caatcatctt cctcgtctca cgagcagaca agatacttca
E--> 146 601 ggagagtttt ctgtgcctc acctgaacgc ctctctgtat cttctactat cgctggggga
E--> 147 661 aagcgcttc cctattcatc agatgtcaat caatcaccaa atagaaggat tgtggatcct
E--> 148 721 gttggactcg ggaatgtagc ttggaaggag agagttgatg gctggaaaat gaagcaagag
E--> 149 781 aagaatactg gtctgtcag cacgcaggct gcttctgaaa gaggtggagt agatattgat
E--> 150 841 gccagcacag atatcctagc agatgaggct ctgctgaatg acgaagcgag gcagcctctg
E--> 151 901 tcaaggaaaag tttcaattcc ttcatacagg atcaatcctt acagaatggt tattatgctg
E--> 152 961 cggtttgtta tcctttgtct cttcttgcac taccgtataa caaacccagt gccaaatgcc
E--> 153 1021 tttgctctat ggctggtctc tgtgatatgt gagatctggt ttgccttacc ctggattttg
E--> 154 1081 gatcagtttc ccaagtgggt tcctgtgaac cgtgaaacct acctcgacag gcttgcctta
E--> 155 1141 agatatgac gtgaagggtga gccatcacag ttagctgctg ttgacatttt cgtgagtact
E--> 156 1201 gttgaccctc tgaaggagcc accccttctg acagccaaca cagtgccttc tattctggct
E--> 157 1261 gttgactacc cagttgacaa ggtgtcctgt tatgtttttg atgatgggtc tgctatgtta
E--> 158 1321 tcatttgaat cacttgcaga aacatcacag tttgctcgta aatgggtacc attttgcaag
E--> 159 1381 aaatatagca tagagcctcg tgcaccagaa tggtaacttg ctgcgaaaat agattacttg
E--> 160 1441 aaggataaag ttcagacatc atttgtcaaa gatcgtagag ctatgaagag ggaatatgag
E--> 161 1501 gaatttaaaa tccgaatcaa tgcacttggt tccaaagccc taaaatgtcc tgaagaaggg
E--> 162 1561 tgggttatgc aagatggcac accgtggcct ggaaataata caggggacca tccaggaatg
E--> 163 1621 atccaggtct tcttagggca aaatggtgga cttgatgcag agggcaatga gctcccgcgt
E--> 164 1681 ttggtatatg tttctcgaga aaagcgacca ggattccagc accacaaaaa ggctgggtgt
E--> 165 1741 atgaatgcac tgggtgagagt ttcagcagtt cttaccaatg gacctttcat cttgaatctt
E--> 166 1801 gattgtgatc attacataaa taacagcaaa gccttaagag aagcaatgtg cttcctgatg

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RAW SEQUENCE LISTING

DATE: 07/18/2002

PATENT APPLICATION: US/09/686,234A

TIME: 13:16:40

Input Set : A:\EP.txt

Output Set: N:\CRF3\07182002\I686234A.raw

Summary

E--> 167	1861	gacccaaacc	tcgggaagca	agtttggtat	gttcagttcc	cacaaagatt	tgatggtatc
E--> 168	1921	gataagaacg	atagatatgc	taatcgtaat	accgtgttct	ttgatattaa	cttgagaggt
E--> 169	1981	ttagatggga	ttcaaggacc	tgtatatgtc	ggaactggat	gtgttttcaa	cagaacagca
E--> 170	2041	ttatacgggt	atgaacctcc	aataaaaagta	aaacacaaga	agccaagtct	tttatctaag
E--> 171	2101	ctctgtggtg	gatcaagaaa	gaagaattcc	aaagctaaga	aagagtcgga	caaaaagaaa
E--> 172	2161	tcaggcaggc	atactgactc	aactgttcct	gtattcaacc	tcgatgacat	agaagagggg
E--> 173	2221	gttgaagggtg	ctgggtttga	tgatgaaaag	gcgctcttaa	tgtcgcaaat	gagcctggag
E--> 174	2281	aagcgatttg	gacagtctgc	tggttttggt	gcttctaccc	taatggaaaa	tggtggtggt
E--> 175	2341	cctccttcag	caactccaga	aaaccttctc	aaagaggcta	tccatgtcat	tagttgtggt
E--> 176	2401	tatgaggata	agtcagattg	gggaatggag	attggatgga	tctatgggtc	tgtgacagaa
E--> 177	2461	gatattctga	ctgggttcaa	aatgcatgcc	cgtggatggc	gatccattta	ctgcatgcct
E--> 178	2521	aagcttccag	ctttcaaggg	ttctgtctct	atcaatcttt	cagatcgtct	gaaccaagtg
E--> 179	2581	ctgaggtggg	cttttaggttc	agttgagatt	ctcttcagtc	ggcattgtcc	tatatggtat
E--> 180	2641	ggttacaatg	ggaggctaaa	atttcttgag	aggtttgcgt	atgtgaacac	caccatctac
E--> 181	2701	cctatcacct	ccattcctct	tctcatgtat	tgtacattgc	tagccgtttg	tctcttcacc
E--> 182	2761	aaccagttta	ttattcctca	gattagtaac	attgcaagta	tatggtttct	gtctctcttt
E--> 185	2821	ctctccattt	tcgccacggg	tatactagaa	atgaggtgga	gtggcgtagg	catagacgaa
E--> 186	2881	tggtggagaa	acgagcagtt	ttgggtcatt	ggtggagtat	ccgctcattt	attcgtctgtg
E--> 187	2941	tttcaaggta	tcctcaaagt	ccttgccggg	attgacacaa	acttcacagt	tacctcaaaa
E--> 188	3001	gcttcagatg	aagacggaga	ctttgctgag	ctctacttgt	tcaaatggac	aacacttctg
E--> 189	3061	attccgccaa	cgacgctgct	cattgtaaac	ttagtgggag	ttgttgccag	agtctcttat
E--> 190	3121	gctatcaaca	gtggatacca	atcatgggga	ccactctttg	ataagttggt	ctttgccttc
E--> 191	3181	tgggtgattg	ttcacttgta	ccctttcctc	aagggtttga	tgggtcgaca	gaaccggact
E--> 192	3241	cctaccattg	ttgtggtctg	gtctgttctc	ttggcttcta	tcttctcggt	gttggtgggt
E--> 193	3301	aggattgata	ccttcactag	ccgagtcact	ggcccgga	ttctggaatg	tggaatcaac
E--> 194	3361	tgttgagaag	cgagcaaata	tttacctgtt	ttgaggggta	aaaaaaacac	agaatttaaa
E--> 195	3421	ttatttttca	ttgtttttatt	tgttcacttt	tttacttttg	ttgtgtgtat	ctgtctgttc
E--> 196	3481	gttcttctgt	cttggtgtca	taaatttatg	tgtagaatat	atcttactct	agttactttg
E--> 197	3541	gaaagttata	attaaagtga	aag			

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/686,234A

DATE: 07/18/2002

TIME: 13:16:41

Input Set : A:\EP.txt

Output Set: N:\CRF3\07182002\I686234A.raw

L:18 M:220 C: Keyword misspelled or invalid format, [(F) ZIP:]
L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:36 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]
L:52 M:220 C: Keyword misspelled or invalid format, [(ii) MOLECULE TYPE:]
L:60 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:60 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:61 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:61 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:61 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:62 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:62 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:62 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:63 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:63 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:63 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:64 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:64 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:64 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:65 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:65 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:65 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:66 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:66 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:66 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:67 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:67 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:67 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:68 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:68 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:68 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:69 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:69 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:69 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:70 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:70 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:70 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:71 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:71 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:71 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:72 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:72 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:73 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:73 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:73 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:74 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:74 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7

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Input Set : A:\EP.txt

Output Set: N:\CRF3\07182002\I686234A.raw

L:74 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:75 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:75 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:75 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:76 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:76 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:76 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:77 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:77 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:77 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:78 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:78 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:78 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:79 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:79 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:79 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:80 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:80 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:80 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:81 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:81 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:81 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:82 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:82 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:82 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:83 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:83 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:84 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:84 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:84 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:85 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:85 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:85 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:86 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:86 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:86 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:87 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:87 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:87 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:88 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:88 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:88 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:89 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:89 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:89 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:90 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:90 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:90 M:333 E: Wrong sequence grouping, Amino acids not in groups!

VERIFICATION SUMMARY

DATE: 07/18/2002

PATENT APPLICATION: US/09/686,234A

TIME: 13:16:41

Input Set : A:\EP.txt

Output Set: N:\CRF3\07182002\I686234A.raw

L:91 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:91 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:91 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:92 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:92 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:92 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:93 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:93 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:93 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:94 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:94 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:94 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:95 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:95 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:95 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:96 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:96 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:96 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:97 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:97 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:97 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:98 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:98 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:98 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:99 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:99 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:100 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:100 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:100 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:101 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:101 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:102 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:102 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:102 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:103 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:103 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:103 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:104 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:104 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:105 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:105 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:106 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:106 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:106 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0

VERIFICATION SUMMARY

DATE: 07/18/2002

PATENT APPLICATION: US/09/686,234A

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Input Set : A:\EP.txt

Output Set: N:\CRF3\07182002\I686234A.raw

L:107 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:107 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:108 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:108 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:109 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:109 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:119 M:204 E: No. of Bases differ, LENGTH:Input:3563 Counted:0 SEQ:1
L:197 M:204 E: No. of Bases differ, LENGTH:Input:3563 Counted:0 SEQ:2